



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 145310

TO: Nita M Minnifield
Location: REM-3C01/3C18
Art Unit: 1645
Thursday, February 17, 2005

Case Serial Number: 09/298523

From: Noble Jarrell
Location: Biotech-Chem Library
Rem 1B71
Phone: 272-2556

Noble.jarrell@uspto.gov

Search Notes

*Reviewed
3/3/05
mm*

145310

STIC-Biotech/ChemLib

From: Chan, Christina
Sent: Wednesday, February 16, 2005 9:28 AM
To: Minnifield, Nita; STIC-Biotech/ChemLib
Subject: RE: rush interference sequence search

Please rush. Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

-----Original Message-----

From: Minnifield, Nita
Sent: Wednesday, February 16, 2005 9:16 AM
To: Chan, Christina
Subject: rush interference sequence search

Christina, please approve, AF.

STIC

09/298523

Please do an interference sequence search on SEQ ID NO: 13 (aa) of this application.

Please provide a paper copy of the results.

Thanks,
Minnifield
71976
Art Unit 1645
Office REM-3C01
Mailbox REM-3C18
571-272-0860

STAFF USE ONLY

Searcher: Hoble
Searcher Phone: 2-
Date Searcher Picked up: 2/17/05
Date Completed: 3
Searcher Prep/Rev. Time: 3
Online Time: 3

Type of Search
NA Sequence: # 1
AA Sequence: # 1
Structure: # 1
Bibliographic: 1
Litigation: 1
Patent Family: 1
Other: 1

Vendors and cost where applicable
STN: 1
DIALOG: 1
QUESTEL/ORBIT: 1
LEXIS/NEXIS: 1
SEQUENCE SYSTEM: Compu
WWW/Internet: 1
Other(Specify): 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 17, 2005, 01:09:58 / Search time 133 Seconds

(without alignments)
1260.318 Million cell updates/sec

Title: US-09-298-523D-13

Perfect score: 2546
Sequence: 1 MFASKSRKRVHSIRKFSVG.....NRLTQQQPKTKRKAPSPRP 513

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1376875 seqs, 326749119 residues

Total number of hits satisfying chosen parameters: 1376875

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Published Applications AA*

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2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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5: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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20: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2546	100.0	693	10	Sequence 185, App
2	2546	100.0	693	15	Sequence 10, Appl
3	2546	100.0	693	17	Sequence 4598, Ap
4	2516	98.8	511	9	Sequence 13, Appl
5	2516	98.8	511	10	Sequence 13, Appl
6	2505	98.4	513	9	Sequence 12, Appl
7	2505	98.4	513	10	Sequence 12, Appl
8	2366	92.9	655	10	Sequence 2, Appl
9	2366	92.9	655	16	Sequence 2, Appl
10	2268	88.1	460	10	Sequence 38, Appl
11	2268	88.1	460	16	Sequence 38, Appl
12	2251	88.4	459	10	Sequence 39, Appl
13	2251	88.4	459	16	Sequence 39, Appl

14	2210	86.8	446	14	US-10-254-995-9	Sequence 9, Appl
15	2193	86.1	446	14	US-10-254-995-6	Sequence 6, Appl
16	2119	83.2	451	9	US-09-748-875-67	Sequence 67, Appl
17	2119	83.2	451	10	US-09-298-523B-67	Sequence 67, Appl
18	2117	83.2	428	10	US-09-056-019-24	Sequence 24, Appl
19	2117	83.2	428	16	US-10-751-702-24	Sequence 24, Appl
20	1995	78.4	406	10	US-09-056-019-1	Sequence 1, Appl
21	1995	78.4	406	16	US-10-751-702-1	Sequence 1, Appl
22	1796.5	70.6	487	15	US-10-333-120A-9	Sequence 9, Appl
23	1787.5	70.2	487	10	US-09-748-875-9	Sequence 9, Appl
24	1787.5	70.2	487	10	US-09-298-523B-9	Sequence 9, Appl
25	1771.5	69.6	487	9	US-09-748-875-66	Sequence 66, Appl
26	1771.5	69.6	487	10	US-09-298-523B-66	Sequence 66, Appl
27	1756	69.0	701	15	US-10-282-122A-74228	Sequence 74228, A
28	1752	68.8	701	15	US-10-333-120A-7	Sequence 7, Appl
29	1744	68.5	581	9	US-09-748-875-56	Sequence 56, Appl
30	1744	68.5	581	10	US-09-298-523B-56	Sequence 56, Appl
31	1741	68.4	483	9	US-09-748-875-10	Sequence 10, Appl
32	1741	68.4	483	10	US-09-298-523B-10	Sequence 10, Appl
33	1726	67.8	481	9	US-09-748-875-6	Sequence 6, Appl
34	1726	67.8	481	10	US-09-298-523B-6	Sequence 6, Appl
35	1705.5	67.0	496	9	US-09-748-875-4	Sequence 4, Appl
36	1705.5	67.0	496	10	US-09-298-523B-4	Sequence 4, Appl
37	1653	64.9	437	16	US-10-751-702-40	Sequence 40, Appl
38	1635.5	64.2	488	15	US-10-333-120A-5	Sequence 5, Appl
39	1585.5	62.3	478	9	US-09-748-875-65	Sequence 65, Appl
40	1585.5	62.3	478	10	US-09-298-523B-65	Sequence 65, Appl
41	1581	62.1	663	9	US-09-748-875-58	Sequence 58, Appl
42	1581	62.1	663	10	US-09-298-523B-58	Sequence 58, Appl
43	1581	62.1	663	10	US-09-056-019-8	Sequence 8, Appl
44	1581	62.1	663	10	US-09-969-748C-14	Sequence 14, Appl
45	1581	62.1	663	10	US-09-949-039-104	Sequence 104, App

ALIGNMENTS

RESULT 1
US-09-769-787-185
Sequence 185, Application US/09769787
Publication No. US20030091577A1
GENERAL INFORMATION:
APPLICANT: Microbial Technique Limited
APPLICANT: Gilbert, Christophe PG
APPLICANT: Hansbro, Philip M
TITLE OF INVENTION: Proteins
FILE REFERENCE: PWC/P21129WO
CURRENT APPLICATION NUMBER: US/09/769,787
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: GB 9816337.1
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: US 60/125164
PRIOR FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 388
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 185
LENGTH: 693
TYPE: PRT
ORGANISM: Streptococcus pneumoniae
US-09-769-787-185

Query Match 100.0%, Score 2546, DB 10, Length 693,
Best Local Similarity 100.0%, Pred. No. 1.8e-107,
Matches 513, Conservative 0, Mismatches 0, Indels 0, Gaps 0,
DB 61
61 GEOPKLDSEDDKARKVEYVYKIVGSYAKSTGRTTIVAVLNEANIKNTYANKIV 120
1 MFASKSRKRVHSIRKFSVGASVAVSLVWGSVVAHATENSGATOVPTSSRNANSQAKO 60
1 MFASKSRKRVHSIRKFSVGASVAVSLVWGSVVAHATENSGATOVPTSSRNANSQAKO 60
61 GEOPKLDSEDDKARKVEYVYKIVGSYAKSTGRTTIVAVLNEANIKNTYANKIV 120
61 GEOPKLDSEDDKARKVEYVYKIVGSYAKSTGRTTIVAVLNEANIKNTYANKIV 120

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OM protein - protein search, using sw model

Run on: February 17, 2005, 00:41:26 ; Search time 43 Seconds
(without alignments)
890.561 Million cell updates/sec

Title: US-09-298-523D-13

Perfect score: 2546

Sequence: 1 MPASKEKHYKYSIRKPSVG.....NRLTQOQPPKTKRQPSPTP 513

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/1aa/6C_COMB.pep:*

6: /cgn2_6/ptodata/1/1aa/6D_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2210	86.8	446	US-09-286-981B-9	Sequence 9, Appl
2	2193	86.1	446	US-09-286-981B-6	Sequence 6, Appl
3	1754	68.9	564	US-09-308-022-6	Sequence 6, Appl
4	1524	59.9	406	US-09-286-981B-18	Sequence 18, Appl
5	1517.5	59.6	631	US-08-847-065-25	Sequence 25, Appl
6	1517.5	59.6	631	US-08-829-382-25	Sequence 25, Appl
7	1467	57.6	426	US-09-286-981B-12	Sequence 12, Appl
8	1459	57.3	426	US-09-286-981B-13	Sequence 13, Appl
9	1458	57.3	424	US-09-286-981B-14	Sequence 14, Appl
10	1452	57.0	428	US-09-286-981B-7	Sequence 7, Appl
11	1443.5	56.7	425	US-09-286-981B-11	Sequence 11, Appl
12	1428	56.1	412	US-09-286-981B-17	Sequence 17, Appl
13	1417	55.7	414	US-09-286-981B-16	Sequence 16, Appl
14	1416	55.6	419	US-09-286-981B-15	Sequence 15, Appl
15	1413	55.5	414	US-09-286-981B-10	Sequence 10, Appl
16	1410.5	55.4	431	US-09-286-981B-3	Sequence 3, Appl
17	1373	53.9	453	US-08-961-083-38	Sequence 38, Appl
18	1373	53.9	453	US-09-536-784-38	Sequence 38, Appl
19	1306.5	51.3	413	US-09-286-981B-5	Sequence 5, Appl
20	1233	48.4	864	US-08-714-741-40	Sequence 40, Appl
21	1168.5	45.9	588	US-08-714-741-42	Sequence 42, Appl
22	915.5	36.0	605	US-08-714-741-46	Sequence 46, Appl
23	904.5	35.5	222	US-09-107-433-4344	Sequence 4344, Ap
24	879.5	34.5	216	US-09-583-110-4344	Sequence 4344, Ap
25	854	33.5	8991	US-08-714-741-32	Sequence 32, Appl
26	775.5	30.5	1231	US-08-714-741-41	Sequence 41, Appl
27	770	30.2	275	US-09-583-110-4347	Sequence 4347, Ap

28	757.5	29.8	623	4	US-08-714-741-47	Sequence 47, Appl
29	714	28.0	251	4	US-09-286-981B-4	Sequence 4, Appl
30	657	25.8	233	4	US-09-107-433-3526	Sequence 3526, Ap
31	636	25.0	142	3	US-08-847-065-21	Sequence 21, Appl
32	636	25.0	142	4	US-08-829-382-21	Sequence 21, Appl
33	595	23.4	131	4	US-08-529-055-56	Sequence 56, Appl
34	576.5	22.6	128	4	US-08-529-055-57	Sequence 57, Appl
35	561.5	22.1	482	4	US-09-107-433-4705	Sequence 4705, Ap
36	560	22.0	219	4	US-09-286-981B-8	Sequence 8, Appl
37	542	21.3	114	4	US-09-286-981B-19	Sequence 19, Appl
38	541	21.2	110	3	US-08-961-083-102	Sequence 102, App
39	541	21.2	110	4	US-09-536-784-102	Sequence 102, App
40	497	19.5	695	1	US-08-127-492A-23	Sequence 23, Appl
41	497	19.5	695	1	US-08-482-847-23	Sequence 23, Appl
42	496	19.5	619	1	US-08-463-746-2	Sequence 2, Appl
43	496	19.5	619	1	US-08-214-164-2	Sequence 2, Appl
44	496	19.5	619	2	US-08-467-852A-3	Sequence 3, Appl
45	496	19.5	619	2	US-08-246-636-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-286-981B-9

/ Sequence 9, Application US/09286981B

/ Patent No. 6503511

/ GENERAL INFORMATION:

/ APPLICANT: Wizenand, Theresa M.

/ APPLICANT: Johnson, Leslie S

/ TITLE OF INVENTION: Derivatives of Choline Binding Proteins for Vaccines

/ FILE REFERENCE: 469201-396

/ CURRENT FILING DATE: 1999-04-06

/ PRIOR APPLICATION NUMBER: US 60/085,743

/ PRIOR FILING DATE: 1998-05-15

/ NUMBER OF SEQ ID NOS: 38

/ SOFTWARE: Patent Ver. 2.1

/ SEQ ID NO 9

/ LENGTH: 446

/ TYPE: RNA

/ ORGANISM: Streptococcus pneumoniae

US-09-286-981B-9

Query Match
Best Local Similarity 86.8%, Score 2210, DB 4, Length 446;
Matches 446; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	38	TENEGATQVPTSSNRANSGAEOGROPKCLDSEDAKAEVYVKTVGSSYAKTKCR	97
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QY	98	HTITVALVNEANNIKNEYIKTVESTSBSQQLIMMSRSKYDEAVSFKEDSSSSSSSD	157
DB	61	HTITVALVNEANNIKNEYIKTVESTSBSQQLIMMSRSKYDEAVSFKEDSSSSSSSD	120
QY	158	SSTKEPADTAKPNKPTPEGRKVAEAKKVEBAEKKAQOEEDRRNPTITTKTLEI	217
DB	121	SSTKEPADTAKPNKPTPEGRKVAEAKKVEBAEKKAQOEEDRRNPTITTKTLEI	180
QY	218	ASDVEYKKAELVYKVAKPRDOKTKOAEAVESQOATATKTKTBRERERAK	277
DB	191	ASDVEYKKAELVYKVAKPRDOKTKOAEAVESQOATATKTKTBRERERAK	240
QY	278	RRADAKGQKPRGAKRGVPELATPDCKENDAKSSDSVGEETLPSPLPKEKVAEAE	337
DB	241	RRADAKGQKPRGAKRGVPELATPDCKENDAKSSDSVGEETLPSPLPKEKVAEAE	300
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DB	301	KKVEBAKKKAADQKEEDRRNPTITTKTLEIASDVEYKKAELVYKBAKPRNEEK	360